SEQUENCE LISTING

<110> Andrade-Gordon, Patricia Darrow, Andrew Qi, Jenson

<120> DNA encoding the human serine protease T

<130> ORT-1032

<140>

<141>

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 1

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tcctgctgct gctgtttt gggtctcaga gggccaaggc agcacagcc tgtggtcgcc 120

ccaggatgct gaaccgaatg gtgggcggc aggacacgca ggagggcgag tggccctggc 180

aagtcagcat ccagcgcaac ggaagccact tctgcggggg cagcctcatc gcggagcagt 240

gggtcctgac ggctgcgcac tgcttccgca acacctctga gacgtccctg taccaggtcc 300

tgctgggggc aagg caacccctg taccagggca cggctccag cgctgacgtg gccctggtgg 420

aggtggagag caaccccctg taccagggca cggctccag cgctgacgtg gccctggtgg 420

agactggaggc accagtgce treaceatt acatectece egtgtgetgg ectgacect 480

cggtgatett tgagacggc atgaactget gggtcactgg etggggcagc eccagtgagg 540

aagactcet gecegaaceg eggatectge agaaactege tgtgcecate ategacacae 600

ccaagtgcaa ectgetetae agcaaagaca eegagtttgg etaccaacee aaaaceatea 660

agaatgacat getgtgegee ggettegagg agggcaagaa ggatgeetge aagggegaet 720

cgggeggeece ectggtgtge etegtgggte agtegtgget geaggegggg gtgateaget 780

ggggtgaggg etgtgeege eagaacegee eaggtgteta eatecgtgte accgecace 840

acaactggat ecateggate ateceeaaae tgcagtteea gecagegagg ttgggeggee 900

agaagtgaga ecceegggge eagaageeee ttgaggteea ectggagee ecaceagaet 1020

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<210> 2

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 2

<213> Artificial Sequence

gccaggcctg agga catgag	20
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<220>	
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tgcgctggat gctgacttgc	20
<210> 4	·
<211> 40	
<212> DNA	

<210> 6

<211> 30

<220>	
<223> Description of Artificial Sequence: Nested probe	
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<212> DNA

<213> Artificial Sequence

. <220>

<223> Description of Artificial Sequence: PCR primer

<400> 6

ggggtctaga cttctggccg cccaacctcg

30

<210> 7

<211> 290

<212> PRT

<213> Homo sapiens

<400> 7

Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Cys Phe Gly

1

5

10

15

Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu

20

Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp

Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu
50 55 60

Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr

70 75 80

Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val

85 90 95

Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser

Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val

Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys

130 135 140

Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val

Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg

Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn

Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile

Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala
210 215 220

Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser

225 230 235 240

Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln

245

250

255

Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile

260

265

270

His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly

275

280

285

Gln Lys

290

<210> 8

<211> 1130

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion gene of

Protease T in a zymogen activation vector

<400> 8

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cggccgcttc cctttagtga gggttaatgc ttcgagcaga catgataaga tacattgatg

1020

agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt gaaatttgtg

1080

atgctattgc tttatttgta accattataa gctgcaataa acaagttgac

1130

<210> 9

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein of Protease T in a zymogen activation construct

<400> 9

Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu

•

10

15

Val Val Ser Asn Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys

Asp Asp Asp Val Asp Ala Ala Leu Ala Ala Pro Phe Asp Asp

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Glu Glu Trp Pro

Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser

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Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn

Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu

Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu

Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu

Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val

145 150 155 160

Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp

Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro

Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys

195 200 205

Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr

Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp

225 230 235 240

Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln
245 250 255

Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg

Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp
275 280 285

Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly
290 295 300

Gly Gln Lys Ser Arg His His His His His His 305 310 315